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RAW SEQUENCE LISTING

DATE: 05/07/2002

PATENT APPLICATION: US/10/023,530

TIME: 14:40:53

Input Set : A:\B4717A-US.ST25.txt

Output Set: N:\CRF3\05072002\J023530.raw

3 <110> APPLICANT: LEGRAIN, Pierre
 4 BENAROUS, Richard
 5 BLOT, Guillaume
 6 LASSOT, Irina
 9 <120> TITLE OF INVENTION: PROTEINS THAT INTERACT WITH BETA TrCP
 11 <130> FILE REFERENCE: B4717A
 W--> 12 <140> CURRENT APPLICATION NUMBER: 10/023,530
 C--> 13 <141> CURRENT FILING DATE: 2002-04-22
 15 <150> PRIOR APPLICATION NUMBER: 60/256,276
 16 <151> PRIOR FILING DATE: 2000-12-18
 18 <160> NUMBER OF SEQ ID NOS: 30
 20 <170> SOFTWARE: PatentIn version 3.1
 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 657
 24 <212> TYPE: DNA
 25 <213> ORGANISM: Homo sapiens
 27 <220> FEATURE:
 28 <221> NAME/KEY: gene
 29 <222> LOCATION: (1)..(657)
 30 <223> OTHER INFORMATION: Beta TrCP
 33 <400> SEQUENCE: 1
 34 atggaccggg cggaggcggt gctgcaagag aaggcactca agtttatgaa ttccctcagag 60
 36 agagaagact gtaataatgg cgaaccccct aggaagataa taccagagaa gaattcactt 120
 38 agacagacat acaacagctg tgccagactc tgcttaaacc aagaaacagt atgttttagca 180
 40 agcactgcta tgaagactga gaattgtgtg gccaaaacaa aacttgccaa tggcacttcc 240
 42 agtatgattg tgcccaagca acggaaactc tcagcaagct atgaaaagga aaaggaactg 300
 44 tgtgtcaa atctttgagca gtggtcagag tcagatcaag tgggaatttgt ggaacatctt 360
 46 atatcccaaa tgtgtcatta ccaacatggg cacataaact cgtatcttaa acctatgttg 420
 48 cagagagatt tcataactgc tctgccagct cggggatttg atcatatcgc tgagaacatt 480
 50 ctgtcatacc tggatgccaa atcactatgt gctgctgaac ttgtgtgcaa ggaatggtac 540
 52 cgagtgaact ctgatggcat gctgtggaag aagcttatcg agagaatggt caggacagat 600
 54 tctctgtgga gaggcctggc agaacgaaga ggatggggac agtattttatt caaaaac 657
 57 <210> SEQ ID NO: 2
 58 <211> LENGTH: 219
 59 <212> TYPE: PRT
 60 <213> ORGANISM: Homo sapiens
 62 <220> FEATURE:
 W--> 63 <221> NAME/KEY: BetaTrCP
 64 <222> LOCATION: (1)..(219)
 65 <223> OTHER INFORMATION: F-box protein
 68 <400> SEQUENCE: 2
 70 Met Asp Pro Ala Glu Ala Val Leu Gln Glu Lys Ala Leu Lys Phe Met
 71 1 5 10 15

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74 Asn Ser Ser Glu Arg Glu Asp Cys Asn Asn Gly Glu Pro Pro Arg Lys
75          20          25          30
78 Ile Ile Pro Glu Lys Asn Ser Leu Arg Gln Thr Tyr Asn Ser Cys Ala
79          35          40          45
82 Arg Leu Cys Leu Asn Gln Glu Thr Val Cys Leu Ala Ser Thr Ala Met
83          50          55          60
86 Lys Thr Glu Asn Cys Val Ala Lys Thr Lys Leu Ala Asn Gly Thr Ser
87 65          70          75          80
90 Ser Met Ile Val Pro Lys Gln Arg Lys Leu Ser Ala Ser Tyr Glu Lys
91          85          90          95
94 Glu Lys Glu Leu Cys Val Lys Tyr Phe Glu Gln Trp Ser Glu Ser Asp
95          100          105          110
98 Gln Val Glu Phe Val Glu His Leu Ile Ser Gln Met Cys His Tyr Gln
99          115          120          125
102 His Gly His Ile Asn Ser Tyr Leu Lys Pro Met Leu Gln Arg Asp Phe
103          130          135          140
106 Ile Thr Ala Leu Pro Ala Arg Gly Leu Asp His Ile Ala Glu Asn Ile
107 145          150          155          160
110 Leu Ser Tyr Leu Asp Ala Lys Ser Leu Cys Ala Ala Glu Leu Val Cys
111          165          170          175
114 Lys Glu Trp Tyr Arg Val Thr Ser Asp Gly Met Leu Trp Lys Lys Leu
115          180          185          190
118 Ile Glu Arg Met Val Arg Thr Asp Ser Leu Trp Arg Gly Leu Ala Glu
119          195          200          205
122 Arg Arg Gly Trp Gly Gln Tyr Leu Phe Lys Asn
123          210          215

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126 <210> SEQ ID NO: 3

127 <211> LENGTH: 1680

128 <212> TYPE: DNA

129 <213> ORGANISM: Homo sapiens

131 <220> FEATURE:

132 <221> NAME/KEY: gene

133 <222> LOCATION: (1)..(1680)

134 <223> OTHER INFORMATION: Ras SF1

137 <400> SEQUENCE: 3

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138 ccggggcggt ggttggcggc tacggacgcg caggactggg ggacgggcggt gtacggctat      60
140 gggcgaggcg gaggcgcctt ctttcgaaat gacctggagc agcacgacga gcagtggcta      120
142 ctgcagccaa gaggactcgg actcggagct cgagcagtac ttcaccgcgc gaacctcgct      180
144 agctcgcagg ccgcgcgggg accaggacga gcctgtggag tgggagacac ctgacctttc      240
146 tcaagctgag attgagcaga agatcaagga gtacaatgcc cagatcaaca gcaacctctt      300
148 catgagcttg aacaaggacg gttcttacac aggcttcacg aaggttcagc tgaagctggt      360
150 gcgccctgtc tctgtgcctt ccagcaagaa gccacctcc ttgcaggatg cccggcgggg      420
152 cccaggacgg ggcacaagtg tcaggcgccg cacttccctt tacctgcccc aggatgctgt      480
154 caagcacctg catgtgctgt cagcacaag ggcaagtga gtcattgagg cctgctgcg      540
156 aaagtctctg gtggtggatg acccccgcaa gtttgactc tttgagcgcg ctgagcgta      600
158 cggccaagtg tacttgcgga agctgttgga tgatgagcag cccctgcggc tgcggctcct      660
160 ggcaggggccc agtgacaagg ccctgagctt tgtcctgaag gaaaatgact ctggggaggt      720
162 gaactgggac gccttcagca tgctgaact acataacttc ctacgtatcc tgcagcgggg      780
164 ggaggaggag cacctccgcc agatcctgca gaagtactcc tattgcgcgc agaagatcca      840

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```

166 agaggccctg cacgcctgcc cccttgggtg acctcttgta cccccagggtg gaaggcagac 900
168 agcaggcagc gccaaagtgcg tgccgtgtga gtgtgacagg gccagtgggg cctgtggaat 960
170 gagtgtgcat ggaggccctc ctgtgctggg ggaatgagcc cagagaacag cgaagtagct 1020
172 tgctccctgt gtccacctat ggggtgtagcc aggtatggct ctgcacccct ctgccctcat 1080
174 tactgggcct tagtgggcca gggctgccct gagaagctgc tccaggcctg cagcaggagt 1140
176 ggtgcagaca gaagtctcct caatttttgt ctcagaagtg aaaatcttgg agaccctgca 1200
178 aacagaacag ggtcatgttt gcagggggtga cggccctcat ctatgaggaa aggttttggg 1260
180 tcttgaatgt ggtctcagga tatccttata agagctaagg gtgggtgctc agaataaggc 1320
182 aggcattgag gaagagtctt ggtttctctc tacagtgcc actcctcaca caccctgagg 1380
184 tcaggaggag ctggctcaca gtacagcatg tgccttaatg cttcatatga ggaggatgtc 1440
186 cctgggccag ggtctgtgtg aatgtgggca ctggccagg ttcatacctt atttgcta 1500
188 caaagccagg gtctctccct cagggtgttt ttatgaagtg cgtgaatgta tgtaatgtgt 1560
190 ggtggcctca gctgaatgcc tctgtgggg aaaggggttg gggtgacagt catcatcagg 1620
192 cctggggctg agagaattgg ctcaataaag atttcaagat ccaaaaaaaaa aaaaaaaaaa 1680

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195 <210> SEQ ID NO: 4

196 <211> LENGTH: 270

197 <212> TYPE: PRT

198 <213> ORGANISM: Homo sapiens

200 <220> FEATURE:

W--> 201 <221> NAME/KEY: RasSF1

202 <222> LOCATION: (1)..(270)

203 <223> OTHER INFORMATION: tumor suppressor

206 <400> SEQUENCE: 4.

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208 Met Gly Glu Ala Glu Ala Pro Ser Phe Glu Met Thr Trp Ser Ser Thr
209 1 5 10 15
212 Thr Ser Ser Gly Tyr Cys Ser Gln Glu Asp Ser Asp Ser Glu Leu Glu
213 20 25 30
216 Gln Tyr Phe Thr Ala Arg Thr Ser Leu Ala Arg Arg Pro Arg Arg Asp
217 35 40 45
220 Gln Asp Glu Pro Val Glu Trp Glu Thr Pro Asp Leu Ser Gln Ala Glu
221 50 55 60
224 Ile Glu Gln Lys Ile Lys Glu Tyr Asn Ala Gln Ile Asn Ser Asn Leu
225 65 70 75 80
228 Phe Met Ser Leu Asn Lys Asp Gly Ser Tyr Thr Gly Phe Ile Lys Val
229 85 90 95
232 Gln Leu Lys Leu Val Arg Pro Val Ser Val Pro Ser Ser Lys Lys Pro
233 100 105 110
236 Pro Ser Leu Gln Asp Ala Arg Arg Gly Pro Gly Arg Gly Thr Ser Val
237 115 120 125
240 Arg Arg Arg Thr Ser Phe Tyr Leu Pro Lys Asp Ala Val Lys His Leu
241 130 135 140
244 His Val Leu Ser Arg Thr Arg Ala Arg Glu Val Ile Glu Ala Leu Leu
245 145 150 155 160
248 Arg Lys Phe Leu Val Val Asp Asp Pro Arg Lys Phe Ala Leu Phe Glu
249 165 170 175
252 Arg Ala Glu Arg His Gly Gln Val Tyr Leu Arg Lys Leu Leu Asp Asp
253 180 185 190
256 Glu Gln Pro Leu Arg Leu Arg Leu Leu Ala Gly Pro Ser Asp Lys Ala
257 195 200 205

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260 Leu Ser Phe Val Leu Lys Glu Asn Asp Ser Gly Glu Val Asn Trp Asp
261      210                      215                      220
264 Ala Phe Ser Met Pro Glu Leu His Asn Phe Leu Arg Ile Leu Gln Arg
265 225                      230                      235                      240
268 Glu Glu Glu Glu His Leu Arg Gln Ile Leu Gln Lys Tyr Ser Tyr Cys
269                      245                      250                      255
272 Arg Gln Lys Ile Gln Glu Ala Leu His Ala Cys Pro Leu Gly
273      260                      265                      270

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276 <210> SEQ ID NO: 5

277 <211> LENGTH: 10

278 <212> TYPE: DNA

279 <213> ORGANISM: Artificial sequence

281 <220> FEATURE:

282 <223> OTHER INFORMATION: linker to clone into pP6 plasmid

284 <220> FEATURE:

W--> 285 <221> NAME/KEY: HGX931

286 <222> LOCATION: (1)..(10)

287 <223> OTHER INFORMATION:

290 <400> SEQUENCE: 5

291 gggccacgaa

10

294 <210> SEQ ID NO: 6

295 <211> LENGTH: 13

296 <212> TYPE: DNA

297 <213> ORGANISM: Artificial sequence

299 <220> FEATURE:

300 <223> OTHER INFORMATION: linker to clone into pP6 plasmid

302 <220> FEATURE:

W--> 303 <221> NAME/KEY: HGX932

304 <222> LOCATION: (1)..(13)

305 <223> OTHER INFORMATION:

308 <400> SEQUENCE: 6

309 ttctgtggccc ctg

13

312 <210> SEQ ID NO: 7

313 <211> LENGTH: 69

314 <212> TYPE: DNA

315 <213> ORGANISM: Artificial sequence

317 <220> FEATURE:

318 <223> OTHER INFORMATION: oligonucleotide used for the construction of pP6 plasmid

320 <220> FEATURE:

W--> 321 <221> NAME/KEY: oligonucleotide

322 <222> LOCATION: (1)..(69)

323 <223> OTHER INFORMATION: 5'-3' single-stranded

324 complementary to sequence ID NO.28

327 <400> SEQUENCE: 7

328 tcgagggggc cccagtggcc cttaattaa ggatccccac tagtgcggcc gcgggccctg

60

331 cggccatgg

69

334 <210> SEQ ID NO: 8

335 <211> LENGTH: 64

336 <212> TYPE: DNA

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Input Set : A:\B4717A-US.ST25.txt

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337 <213> ORGANISM: Artificial Sequence
339 <220> FEATURE:
340 <223> OTHER INFORMATION: oligonucleotide used for the construction of pB6 plasmid
342 <220> FEATURE:
W--> 343 <221> NAME/KEY: oligonucleotide
344 <222> LOCATION: (1)..(64)
345 <223> OTHER INFORMATION: 5'-3' single-stranded
346 Complementary to sequence SEQ ID NO. 29
349 <400> SEQUENCE: 8
350 tcgagggggc cccagtggcc cttaattaa ggatccccac tagtgcggcc gcggcccgtc      60
353 cggc                                     64
356 <210> SEQ ID NO: 9
357 <211> LENGTH: 68
358 <212> TYPE: DNA
359 <213> ORGANISM: Artificial Sequence
361 <220> FEATURE:
362 <223> OTHER INFORMATION: oligonucleotide used for the construction of pB20 plasmid
364 <220> FEATURE:
W--> 365 <221> NAME/KEY: oligonucleotide
366 <222> LOCATION: (1)..(68)
367 <223> OTHER INFORMATION: 5'-3' single-stranded
368 Complementary to SEQ ID NO. 30
371 <400> SEQUENCE: 9
372 ggtcgagggg cccagtggc cttaattaa ggatccccac tagtgcggcc gcggcccgtc      60
375 cgcccccg                                     68
378 <210> SEQ ID NO: 10
379 <211> LENGTH: 20
380 <212> TYPE: DNA
381 <213> ORGANISM: Artificial Sequence
383 <220> FEATURE:
384 <223> OTHER INFORMATION: primer used in PCR on yeast colonies
386 <220> FEATURE:
W--> 387 <221> NAME/KEY: ABS1
388 <222> LOCATION: (1)..(20)
389 <223> OTHER INFORMATION: PCR primer
392 <400> SEQUENCE: 10
393 gcgtttggaa tcactacagg                                     20
396 <210> SEQ ID NO: 11
397 <211> LENGTH: 19
398 <212> TYPE: DNA
399 <213> ORGANISM: Artificial Sequence
401 <220> FEATURE:
402 <223> OTHER INFORMATION: Primer used in PCR on yeast colonies
404 <220> FEATURE:
W--> 405 <221> NAME/KEY: ABS2
406 <222> LOCATION: (1)..(19)
407 <223> OTHER INFORMATION: PCR primer
410 <400> SEQUENCE: 11
411 cacgatgcac gttgaagtg                                     19

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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/023,530

DATE: 05/07/2002

TIME: 14:40:54

Input Set : A:\B4717A-US.ST25.txt

Output Set: N:\CRF3\05072002\J023530.raw

L:12 M:283 W: Missing Blank Line separator, <140> field identifier
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:63 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:2
L:201 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4
L:285 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5
L:303 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:6
L:321 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:7
L:343 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:8
L:365 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:9
L:387 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:10
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L:495 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:17
L:510 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:18
L:525 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:19
L:540 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:20
L:547 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:20
L:562 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:21
L:577 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:22
L:592 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:23
L:607 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:24
L:622 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:25
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L:692 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:29
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